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OM protein - protein search, using sw model

Run on: December 13, 2004, 18:48:47 ; Search time 110.978 Seconds
(without alignments)
426.682 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	692	100.0	132	5	ABG76923	Abg76923 Mouse 3D6
2	655	94.7	238	8	ADM72033	Adm72033 Chimeric
3	653	94.4	238	8	ADP45549	Adp45549 Mouse bin
4	650	93.9	135	5	ABB79729	Abb79729 Anti-Stre
5	644	93.1	239	6	ABP58274	Abp58274 Humanised
6	641	92.6	132	2	AAR12361	Aar12361 Light (ka
7	641	92.6	133	8	ADO00819	Ado00819 Antibody
8	641	92.6	133	8	ADO43845	Ado43845 Light cha
9	640	92.5	132	5	ABG76925	Abg76925 Humanised

10	639	92.3	131	2	AAR12239	Aar12239	Mouse MAb
11	636	91.9	132	6	ABG74244	Abg74244	Mouse ant
12	630	91.0	132	5	ABG76931	Abg76931	Humanised
13	628	90.8	132	2	AAR24712	Aar24712	Sequence
14	606	87.6	142	4	AAE07032	Aae07032	Murine an
15	595	86.0	239	2	AAR24811	Aar24811	Sequence
16	589	85.1	239	7	ADD47025	Add47025	Rat Prote
17	571	82.5	113	4	AAE03751	Aae03751	Murine PS
18	571	82.5	218	4	AAE03756	Aae03756	Chimeric
19	566	81.8	113	8	ADG25828	Adg25828	Anti-CD30
20	566	81.8	114	8	ADG25839	Adg25839	Anti-CD30
21	562	81.2	353	2	AAY06273	Aay06273	Anti Fc a
22	560	80.9	112	4	AAE06946	Aae06946	Murine 1D
23	560	80.9	112	4	AAU09918	Aau09918	Murine mA
24	560	80.9	112	5	ABG75527	Abg75527	Mouse mAb
25	560	80.9	112	5	ADF98231	Adf98231	Murine mA
26	560	80.9	112	7	ABR61865	Abr61865	Mouse MAb
27	560	80.9	112	8	ADQ31246	Adq31246	Murine 1A
28	560	80.9	122	8	ADJ95990	Adj95990	Immunoglo
29	560	80.9	130	8	ADJ95992	Adj95992	Immunoglo
30	560	80.9	238	8	ADM72035	Adm72035	Chimeric
31	560	80.9	257	3	AAB09777	Aab09777	Antiviral
32	559	80.8	112	2	AAY52765	Aay52765	Anti-tiss
33	559	80.8	112	2	AAY52766	Aay52766	Anti-tiss
34	556	80.3	112	4	AAE06991	Aae06991	Human kap
35	555	80.2	112	5	AAO14971	Aao14971	Mouse lig
36	550	79.5	243	2	AAW60769	Aaw60769	Single ch
37	548	79.2	112	2	AAW48248	Aaw48248	A77 anti-
38	548	79.2	112	4	AAB74621	Aab74621	A77 anti-
39	548	79.2	112	4	AAE08554	Aae08554	Murine A7
40	548	79.2	535	2	AAW28491	Aaw28491	Human p53
41	548	79.2	535	2	AAW28492	Aaw28492	Human p53
42	547	79.0	162	7	ADE06760	Ade06760	D13 light
43	546	78.9	112	7	ABR62960	Abr62960	Monoclonal
44	543	78.5	113	6	ABP58270	Abp58270	Humanised
45	543	78.5	219	6	ABP58272	Abp58272	Humanised

ALIGNMENTS

RESULT 1

ABG76923

ID ABG76923 standard; protein; 132 AA.

XX

AC ABG76923;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VL protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation; Abeta.

XX
OS Mus musculus.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
DR WPI; 2002-519658/55.
DR N-PSDB; ABS59426.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 67; Fig 1; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 6e-55;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
||| ||| ||| |||
Db 121 RTFGGGTKLEIK 132

RESULT 2
ADM72033

ID ADM72033 standard; protein; 238 AA.
XX
AC ADM72033;
XX
DT 03-JUN-2004 (first entry)
XX
DE Chimeric mouse-human antibody M3C11 light chain.
XX
KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
KW cytostatic; M3C11.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO2004022739-A1.
XX
PD 18-MAR-2004.
XX
PF 04-SEP-2003; 2003WO-JP011318.
XX
PR 04-SEP-2002; 2002WO-JP008999.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;
XX
DR WPI; 2004-269573/25.
DR N-PSDB; ADM72032.
XX
PT Antibody against the N terminus of glypican 3(GPC3) causes cell
PT disruption and is useful as an anticancer agent.
XX
PS Example 4; SEQ ID NO 18; 122pp; Japanese.
XX
CC The invention relates to an antibody against the N terminus of glypican 3
CC (GPC3). The antibody can be used for causing cell disruption and can be
CC used as an anti-cancer agent. The present sequence represents a chimeric
CC mouse-human antibody M3C11 light chain.
XX
SQ Sequence 238 AA;

Query Match 94.7%; Score 655; DB 8; Length 238;
Best Local Similarity 94.7%; Pred. No. 2.6e-51;
Matches 124; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVIWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWL 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MSPAQFLFLLVIWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWL 60

Qy 62 LQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :||| ||| :||| |||
Db 61 LQRPGQSPKRLIYLVSKLDGAPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGTHFPL 120

Qy 122 TFGGGTKEIK 132
||| ||| :|
Db 121 TFGAGTKLELK 131

RESULT 3

ADP45549

ID ADP45549 standard; protein; 238 AA.

XX

AC ADP45549;

XX

DT 09-SEP-2004 (first entry)

XX

DE Mouse binding molecule 11C7 light chain SEQ ID NO:3.

XX

KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW mouse; antibody.

XX

OS Mus musculus.

XX

PN WO2004052932-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-EP013960.

XX

PR 10-DEC-2002; 2002GB-00028832.

XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.

PA (UYZU-) UNIV ZUERICH.

XX

PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;

XX

DR WPI; 2004-468818/44.

XX

PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.

XX

PS Claim 9; SEQ ID NO 3; 121pp; English.

XX

CC The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a CC dissociation constant of less than 1000nM. Also described: (1) a CC polynucleotide encoding the binding molecule; (2) an expression vector or CC system comprising the polynucleotide; (3) a host cell comprising the CC expression system; (4) a pharmaceutical composition comprising the CC binding molecule and a carrier or diluent; and (5) treating diseases CC associated with nerve repair. The binding molecule has neuroprotective CC activity, and can be used in gene therapy. The binding molecule is useful CC in preparing a composition for treating central nervous system (CNS) CC injury or neurodegenerative disorders. The present sequence represents a CC mouse binding molecule 11C7 light chain, which is used in the CC exemplification of the present invention.

XX

SQ Sequence 238 AA;

Query Match 94.4%; Score 653; DB 8; Length 238;
Best Local Similarity 93.9%; Pred. No. 4e-51;
Matches 123; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
|||:|||||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:
Db 1 MSPAQFLFLVLWIRETSGDVLLQTPLTLSITIGQPASISCKSSQSLLHSDGKTYLNWL 60

Qy 62 LQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPQ 120

Qy 122 TFGGGTKEIK 132
|||:|||||:
Db 121 TFGGGTKEIK 131

RESULT 4

ABB79729

ID ABB79729 standard; protein; 135 AA.
XX
AC ABB79729;
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VL.
XX
KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy.
XX
OS Mus musculus.
XX
PN US2002068066-A1.
XX
PD 06-JUN-2002.
XX
PF 15-JUN-2001; 2001US-00881823.
XX
PR 20-AUG-1999; 99US-00378577.
XX
PA (SHIW/) SHI W.
PA (MORR/) MORRISON S L.
PA (TRIN/) TRINH K.
PA (WIMS/) WIMS L.
PA (CHEN/) CHEN L.
PA (ANDE/) ANDERSON M H.
XX
PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX
DR WPI; 2002-565838/60.
DR N-PSDB; ABN84610.
XX
PT Treatment and prevention of dental caries in mammals, in particular
PT humans by orally administering genetically engineered or purified
PT antibodies that bind to surface antigens of carcinogenic organisms.

XX
PS Claim 13; Fig 3A; 30pp; English.
XX

CC The present sequence is the protein sequence of the light chain variable
CC region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of cariogenic type c Streptococcus
CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion

XX
SQ Sequence 135 AA;

Query Match 93.9%; Score 650; DB 5; Length 135;
Best Local Similarity 93.2%; Pred. No. 4e-51;
Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :||| :|||
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLDRDGRTYLSW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :||| :||| :||| |||
Db 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
||| ||| :|||
Db 121 LTFGAGTKLELK 132

RESULT 5

ABP58274

ID ABP58274 standard; protein; 239 AA.

XX
AC ABP58274;

XX
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX

DE Humanised 3D6 antibody light chain.

XX
KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
KW human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.

XX
OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide

FT Protein 21. .239
FT /label= Mature_peptide
FT /note= "the mature light chain is claimed in Claim 5"
FT Region 21. .133
FT /note= "light chain variable region, claimed in Claim 4"
FT Region 44. .59
FT /note= "CDR1"
FT Region 75. .81
FT /note= "CDR2"
FT Region 114. .122
FT /note= "CDR3"
XX
PN WO200288306-A2.
XX
PD 07-NOV-2002.
XX
PF 26-APR-2002; 2002WO-US011853.
XX
PR 30-APR-2001; 2001US-0287539P.
XX
PA (ELI LILLY & CO ELI.
XX
PI Tsurushita N, Vasquez M;
XX
DR WPI; 2003-183835/18.
DR N-PSDB; ABZ24632, ABZ24634.
XX
PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta plaque in the brain.
XX
PS Disclosure; Page 12-13; 54pp; English.
XX
CC The present sequence is that of a preferred light chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline Vk segment DPK19 and J segment Jk4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 239 AA;

Query Match 93.1%; Score 644; DB 6; Length 239;
Best Local Similarity 90.9%; Pred. No. 2.6e-50;
Matches 120; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| :||| :||| :||| ||| ||| ||| ||| ||| |||
Db 1 MMSPAQFLFLVLWIRETNGDVVMTQSPLSLPVTLGQPASISCKSSQSLLSDGKTYLNW 60
Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRRIEAEDLGLYYCWQGTHFP 120
| ||| ||| :||| ||| ||| ||| ||| :||| ||| ||| ||| :||| :||| :||| |||
Db 61 LQQRPGQSPRRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDGVVYCWQGTHFP 120
Qy 121 RTFGGGTKLEIK 132
||| ||| :|||
Db 121 RTFGGGTKVEIK 132

RESULT 6
AAR12361
ID AAR12361 standard; protein; 132 AA.
XX
AC AAR12361;
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX
DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.
XX
KW Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
OS Mus musculus.
XX
PN WO9107493-A.
XX
PD 30-MAY-1991.
XX
PF 13-NOV-1989; 89US-00433730.
XX
PR 13-NOV-1989; 89US-00433730.
XX
PA (XOMA) XOMA CORP.
PA (GREC) GREEN CROSS CORP.
XX
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX
DR WPI; 1991-178105/24.
DR N-PSDB; AAQ12063.
XX
PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX
PS Disclosure; Fig 18; 107pp; English.
XX
CC This is the light (kappa) - chain variable (V) region of a mouse
CC monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral
CC antigen. It is used in the construction of a chimeric MAb comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric Mabs are more effective than murine MAb 4D12 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric Mabs can be

CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
XX

SQ Sequence 132 AA;

Query Match 92.6%; Score 641; DB 2; Length 132;
Best Local Similarity 90.9%; Pred. No. 2.5e-50;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASFCKSSQSLLSDGKTFLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRRIEAEDLGLYYCWQGTHFP 120
Db 61 FLQRPGQSPKRLLYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHFP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 ITFGAGTKLELR 132

RESULT 7

ADO00819

ID ADO00819 standard; protein; 133 AA.

XX

AC ADO00819;

XX

DT 01-JUL-2004 (first entry)

XX

DE Antibody JRF/cAbeta40/10 light chain variable region, SEQ ID 6.

XX

KW Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;
KW beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;
KW cleavage site; immunogen; murine; antibody; light chain; variable region;
KW JRF/cAbeta40/10.

XX

OS Mus sp.

XX

Key	Location/Qualifiers
FT Domain	44. .59
FT	/note= "CDR1"
FT Domain	75. .81
FT	/note= "CDR2"
FT Domain	114. .122
FT	/note= "CDR3"

XX

PN WO2004029629-A1.

XX

PD 08-APR-2004.

XX

PF 27-SEP-2002; 2002WO-EP011062.

XX

PR 27-SEP-2002; 2002WO-EP011062.

XX

PA (JANC) JANSSEN PHARM NV.
XX
PI Mercken MH, Vandermeeren MMPP;
XX
DR WPI; 2004-316180/29.
XX
PT New N-11 truncated amyloid-beta monoclonal antibodies specific for human
PT Amyloid-beta 11 N-terminal site (A-beta11-x peptides), useful for
PT diagnosing or treating beta-amyloid-related diseases e.g. Alzheimer's
PT disease.
XX
PS Disclosure; SEQ ID NO 6; 42pp; English.
XX
CC The present invention relates to an antibody expressed by the hybridoma
CC cells J&JPRD/hAbeta11/1 and J&JPRD/hAbeta11/2, which is capable of
CC specifically recognizing human Amyloid-beta 11 N-terminal site (i.e.,
CC Abeta11-x peptides). The antibody is useful for diagnosing beta-amyloid-
CC related diseases. It is particularly useful for prognosis and monitoring
CC response to therapy of Alzheimer's disease and other beta-amyloid related
CC diseases and in passive immunization as a method for treating such
CC diseases. A humanized form of the antibody is useful for manufacturing a
CC medicament for treating, preventing or reversing cognitive decline in
CC clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary
CC Cerebral Hemorrhage with Amyloidosis of the Dutch-Type, cerebral amyloid
CC angiopathy or other beta-amyloid-related diseases, or to inhibit the
CC formation of amyloid plaques or the effects of toxic soluble Amyloid-beta
CC ; species in humans. It can also be used in assay systems such as
CC competitive methods and nephelometry. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 133 AA;

Query Match 92.6%; Score 641; DB 8; Length 133;
Best Local Similarity 91.7%; Pred. No. 2.6e-50;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| ||| ||| ||| : ||| |||
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLAVTIGQPASISCKSGQSLARDGKTYLSW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
||| ||| ||| ||| ||| ||| ||| ||| : ||| ||| ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKINRVEAEDLGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
||| ||| |||
Db 121 RTFGGGTNLEIK 132

RESULT 8
ADO43845
ID ADO43845 standard; protein; 133 AA.
XX
AC ADO43845;
XX
DT 15-JUL-2004 (first entry)
XX

DE Light chain variable region of anti-amyloid-beta antibody.

XX

KW antibody; Amyloid-beta11-x peptide; BACE-1; amyloid-beta; beta-secretase;

KW beta-amyloid precursor protein; beta-amyloid-related disease;

KW Alzheimer's disease; vaccine; Down's syndrome;

KW hereditary cerebral haemorrhage; amyloidosis;

KW cerebral amyloid angiopathy; amyloid plaque.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Region 44. .59

FT /note= "CDR1"

FT Region 75. .81

FT /note= "CDR2"

FT Region 114. .122

FT /note= "CDR3"

XX

PN WO2004029630-A1.

XX

PD 08-APR-2004.

XX

PF 09-SEP-2003; 2003WO-EP010092.

XX

PR 27-SEP-2002; 2002WO-EP011062.

XX

PA (JANCO) JANSSEN PHARM NV.

XX

PI Mercken MH, Vandermeeren MMPP;

XX

DR WPI; 2004-316181/29.

XX

PT New N-11 truncated amyloid-beta monoclonal antibodies specific for human

PT Amyloid-beta 11-x peptides (A-beta11-x peptides), useful for diagnosing

PT or treating beta-amyloid-related diseases e.g., Alzheimer's disease.

XX

PS Disclosure; Page 38-39; 50pp; English.

XX

CC The specification describes a monoclonal antibody which specifically

CC recognizes human Amyloid-beta11-x peptides. These peptides result from

CC overexpression of BACE-1 which causes additional cleavage at the +11 site

CC of amyloid-beta, generating shorter fragments known as Amyloid-beta11-x

CC peptides. BACE-1 is the major beta-secretase required for cleavage of

CC beta-amyloid precursor protein. The antibody is useful for detecting the

CC presence of amyloid-beta peptides in a tissue or fluid sample and for

CC diagnosing beta-amyloid-related diseases. It is particularly useful for

CC prognosis and monitoring response to therapy of Alzheimer's disease and

CC other beta-amyloid related diseases and in passive immunization as a

CC method for treating such diseases. A humanized form of the antibody is

CC useful for manufacturing a medicament for treating, preventing or

CC reversing cognitive decline in clinical or pre-clinical Alzheimer's

CC Disease, Down's syndrome, Hereditary Cerebral Haemorrhage with

CC Amyloidosis of the Dutch-Type, cerebral amyloid angiopathy or other beta-

CC amyloid-related diseases, or to inhibit the formation of amyloid plaques

CC or the effects of toxic soluble Amyloid-beta species in humans. The

CC present sequence represents the light chain variable region of an

CC antibody that recognises amyloid-beta-40 and amyloid-beta11-x peptide

CC amyloid-beta11-40.

XX

SQ Sequence 133 AA;

Query Match 92.6%; Score 641; DB 8; Length 133;
Best Local Similarity 91.7%; Pred. No. 2.6e-50;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| :|||

Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLAVTIGQPASISCKSGQSLLARDGKTYLSW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
||| ||| ||| ||| ||| ||| ||| :||| ||| ||| ||| :||| :||| ||| :||| ||| |||

Db 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKINRVEAEDLGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
||| ||| |||

Db 121 RTFGGGTNLEIK 132

RESULT 9

ABG76925

ID ABG76925 standard; protein; 132 AA.

XX

AC ABG76925;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 light chain variable region #1.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Ab β a.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX

PN WO200246237-A2.

XX

PD 13-JUN-2002.

XX

PF 06-DEC-2001; 2001WO-US046587.

XX

PR 06-DEC-2000; 2000US-0251892P.

XX

PA (NEUR-) NEURALAB LTD.

PA (AMHP) WYETH.

XX

PI Basi G, Saldanha J, Yednock T;

XX

DR WPI; 2002-519658/55.

XX

PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.

XX

PS Claim 54; Page 154; 171pp; English.

XX

CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention

XX

SQ Sequence 132 AA;

Query Match 92.5%; Score 640; DB 5; Length 132;
Best Local Similarity 90.2%; Pred. No. 3.1e-50;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 MMSPAQFLFLLVLWIRETNGYVVMQTQSPSLPVTGEPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHFP 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
|||||:|||||:|||||

Db 121 RTFGQGTKVEIK 132

RESULT 10

AAR12239

ID AAR12239 standard; protein; 131 AA.

XX

AC AAR12239;

XX

DT 25-MAR-2003 (revised)

DT 19-AUG-1991 (first entry)

XX

DE Mouse MAb 4D12 L chain V region.

XX

KW HIV-1; chimera.

XX

OS Mus sp.

XX

PN WO9107494-A.

XX

PD 30-MAY-1991.

XX

PF 13-NOV-1989; 89US-00433703.

XX

PR 13-NOV-1989; 89US-00433703.

XX

PA (XOMA) XOMA CORP.

PA (GREC) GREEN CROSS CORP.

PA (ZOMA-) ZOMA CORP.

XX

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX

DR WPI; 1991-178106/24.

DR N-PSDB; AAQ12019.

XX

PT New chimeric mouse human antibodies - used in treatment, diagnosis and
PT prophylaxis of HIV infections.

XX

PS Disclosure; Fig 18; 108pp; English.

XX

CC The mouse VL gene product may be used to produce chimeric mouse- human
CC Abs against HIV-1 comprising human Ig constant regions and murine
CC variable regions. These novel sequence are useful in treatment, diagnosis
CC and prophylaxis of HIV infections, and may be produced by a bacterial,
CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 131 AA;

Query Match 92.3%; Score 639; DB 2; Length 131;
Best Local Similarity 91.6%; Pred. No. 3.8e-50;
Matches 120; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|||

Db 1 MMSPAQFLFLLVLWIRETNGDVVMQTPLTLSVTIGQPASFCKSSQSLLSDGKTFLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :||| ||| :||| ||| :|||

Db 61 FLQRPGQSPKRLLYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHFP 120

Qy 121 RTFGGGTKLEI 131

||| ||| :|||

Db 121 ITFGAGTKLEL 131

RESULT 11

ABG74244

ID ABG74244 standard; protein; 132 AA.

XX

AC ABG74244;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3D8 light chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;
KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
KW small cell lung cancer; light chain variable region; mouse.

XX
OS Mus sp.
XX
PN US2002132983-A1.
XX
PD 19-SEP-2002.
XX
PF 10-DEC-2001; 2001US-00006773.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-208946/20.
DR N-PSDB; ABX16570.
XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX
PS Disclosure; Page 13; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC represents the mouse antibody 3D8 light chain variable region
XX
SQ Sequence 132 AA;

Query Match 91.9%; Score 636; DB 6; Length 132;
Best Local Similarity 93.9%; Pred. No. 7.2e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSPAQFLFLLVLWIQETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWL 60

Qy 62 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHFPR 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPH 120

Qy 122 TFGGGTKLEIK 132
|||||:|||||

RESULT 12
ABG76931
ID ABG76931 standard; protein; 132 AA.
XX
AC ABG76931;
XX
DT 05-NOV-2002 (first entry)
XX
DE Humanised 3D6 light chain variable region #2.
XX
KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX
OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
DR WPI; 2002-519658/55.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 55; Page 157; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention
XX
SQ Sequence 132 AA;

Query Match 91.0%; Score 630; DB 5; Length 132;
 Best Local Similarity 89.4%; Pred. No. 2.5e-49;
 Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNW 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTPGEPASISCKSSQSLSDGKTYLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 LLQKPGQSPQRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
 ||||| |||:|||:
 Db 121 RTFGQGTTKVEIK 132

RESULT 13

AAR24712

ID AAR24712 standard; protein; 132 AA.

XX

AC AAR24712;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the genomic FIB1-11 kappa chain variable (VFK) gene.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;

KW antithrombotic agent; myocardial infarction therapy.

XX

OS Mus musculus.

XX

FH	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/label= leader
FT	Region	21..43
FT		/label= Framework Region (FR) 1
FT	Region	44..59
FT		/label= complementarity determining region (CDR) 1
FT	Region	60..74
FT		/label= FR-2
FT	Region	75..81
FT		/label= CDR-2
FT	Region	82..112
FT		/label= FR-3
FT	Region	113..122
FT		/label= CDR-3
FT	Region	123..132
FT		/label= FR-4

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.

XX

PF 17-DEC-1991; 91EP-00121591.

XX
PR 18-DEC-1990; 90JP-00413829.
PR 11-NOV-1991; 91JP-00294464.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Iwasa S, Tada H, Watanabe T;
XX
DR WPI; 1992-209528/26.
DR N-PSDB; AAQ25665.
XX
PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.
XX
PS Example; Fig 1; 87pp; English.
XX
CC A genomic DNA library was prep'd. from mouse anti-human fibrin specific
CC antibody producer hybrid FIB1-11. Screening using a 32P- labeled mouse
CC JK4-5 gene fragment as a hybridisation probe gave three positive
CC recombinant phage clones. Phage clone KE14 was identified as a clone
CC contg. a 15kb fragment coding for the VFK gene. The phage clone KE14 was
CC subcloned in the plasmid vector pUC119 and sequenced. VFK was a
CC functional VK gene formed by recombination between the VK gene belonging
CC to the Subgroup II (VKII) and the JK2 gene (see AAQ25665). (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 132 AA;

Query Match 90.8%; Score 628; DB 2; Length 132;
Best Local Similarity 91.7%; Pred. No. 3.8e-49;
Matches 121; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDDGKTYLNW 60
Db 1 MMSPAQFLFLLVLWIRETNGDVVMAQTPLTLSVTIGQPAPFISCTSSQSLLSDDGKTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
Db 61 LLQRPGQSPKRLIYLVSKLYSGVVPDRFTGSGSGTAFTLKINRVEAEDLGVYYCWQGIHFP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 YTFGGGTKEIK 132

RESULT 14
AAE07032
ID AAE07032 standard; protein; 142 AA.
XX
AC AAE07032;
XX
DT 16-OCT-2001 (first entry)
XX
DE Murine antibody 1D9 kappa light chain variable region.
XX
KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;

KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW inflammatory glomerulopathy; vascular intervention;
KW neointimal hyperplasia; antibody 1D9 kappa light chain variable region.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers
FT Peptide 1. .17
FT /label= Signal_peptide
FT Protein 18. .142
FT /note= "Murine mature antibody 1D9 kappa light chain
FT variable region"
FT Region 18. .130
FT /label= Variable_region
FT Region 131. .142
FT /label= Constant_region

XX

PN WO200157226-A1.

XX

PD 09-AUG-2001.

XX

PF 02-FEB-2001; 2001WO-US003537.

XX

PR 03-FEB-2000; 2000US-00497625.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;

XX

DR WPI; 2001-488888/53.

DR N-PSDB; AAD13177.

XX

PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.

XX

PS Disclosure; Fig 22; 183pp; English.

XX

CC The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE- mediated allergic reaction, shock,

CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is murine antibody 1D9
CC kappa light chain variable region

XX

SQ Sequence 142 AA;

Query Match 87.6%; Score 606; DB 4; Length 142;
Best Local Similarity 93.5%; Pred. No. 4.1e-47;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 LLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSP 69
||||||| | |||||||:| |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 7 LLVLWIRETIGDVVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSP 66

Qy 70 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKL 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 67 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTLK 126

Qy 130 EIK 132
|||

Db 127 EIK 129

RESULT 15

AAR24811

ID AAR24811 standard; protein; 239 AA.

XX

AC AAR24811;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the chimeric kappa chain cDNA (lgkv) contained in
DE pTB1427.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW antithrombotic agent; myocardial infarction therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1. .20

FT /label= leader

FT Region 21. .133

FT /label= V-kappa

FT Misc-difference 130

FT /note= "Alternatively = Glu"

FT Region 134. .239

FT /label= C-kappa

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.
XX
PF 17-DEC-1991; 91EP-00121591.
XX
PR 18-DEC-1990; 90JP-00413829.
PR 11-NOV-1991; 91JP-00294464.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Iwasa S, Tada H, Watanabe T;
XX
DR WPI; 1992-209528/26.
DR N-PSDB; AAQ25691.
XX
PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.
XX
PS Example; Fig 9; 87pp; English.
XX
CC Poly(A)+ RNA was prep'd. from the anti-fibrin chimeric Ab-producing
CC transformant FIB1-H01/X63 and used as a template to clone human C-kappa
CC cDNA, using the oligo-dT (Pharmacia) primer as a primer for first strand
CC cDNA synthesis and the 3'E-kappa and 5'C-kappa primers for the PCR. An
CC amplified DNA fragment of about 0.33kb was isolated and used to create a
CC C-kappa cDNA contg. vector, pTB1394. Using the same technique, with the
CC 3'E-kappa primer as a primer for first strand synthesis and the 5'L-kappa
CC and 3'C-kappa primers for the PCR, an anti-fibrin V-kappa (V-kappa-v)
CC cDNA was amplified. Furthermore, using the 3'E-kappa primer for first
CC strand synthesis and the 5'mV-kappa and 3'mV-kappa primers for the PCR, an
CC anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition, a
CC leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa as a
CC primer for first strand synthesis and the 5'S-kappa and 3'L- kappa
CC primers for the PCR. The amplified gene fragments (L-kappa: V-kappa-v: V-
CC kappa-FIB) were isolated and used to construct respectively plasmids
CC pTB1391, pTB1392, and pTB1393. L-kappa, V- kappa and C-kappa were joined
CC together to give a plasmid, pTB1427, contg. the whole length of the
CC chimeric kappa chain cDNA. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 239 AA;

Query Match 86.0%; Score 595; DB 2; Length 239;
Best Local Similarity 85.6%; Pred. No. 7.3e-46;
Matches 113; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db 1 MMSPAQFLFLVLWIRETRGDIQLAQTPLTFSVTIGQPAFISCTSSQTLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISREREAEDLGLYYCWQGTHFP 120
Db 61 LLQRPGQSPRRLIYLVSKLYSGVPDFRTGSGSGTAFTLKREREAEDLGVYYCWQGIHFP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 YTFGGGKLVIK 132

Search completed: December 13, 2004, 19:13:22
Job time : 113.978 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:05:17 ; Search time 27.3778 Seconds
(without alignments)
319.748 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLVLIWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	649	93.8	131	4	US-09-647-468-163	Sequence 163, App
2	646	93.4	131	4	US-09-647-468-164	Sequence 164, App
3	606	87.6	142	4	US-09-840-459-102	Sequence 102, App
4	606	87.6	142	4	US-09-497-625A-102	Sequence 102, App
5	562	81.2	353	4	US-09-203-958A-4	Sequence 4, Appli
6	560	80.9	112	4	US-09-809-739-11	Sequence 11, Appli
7	560	80.9	112	4	US-09-840-459-9	Sequence 9, Appli
8	560	80.9	112	4	US-09-497-625A-9	Sequence 9, Appli
9	559	80.8	112	4	US-09-647-468-149	Sequence 149, App
10	559	80.8	112	4	US-09-647-468-150	Sequence 150, App
11	556	80.3	112	4	US-09-840-459-54	Sequence 54, Appli

12	556	80.3	112	4	US-09-497-625A-54	Sequence 54, Appl
13	548	79.2	112	2	US-08-678-194-6	Sequence 6, Appl
14	548	79.2	112	3	US-08-890-011-6	Sequence 6, Appl
15	548	79.2	112	3	US-09-262-724-6	Sequence 6, Appl
16	548	79.2	535	3	US-08-983-035A-38	Sequence 38, Appl
17	538	77.7	112	4	US-09-809-739-16	Sequence 16, Appl
18	538	77.7	112	4	US-09-840-459-14	Sequence 14, Appl
19	538	77.7	112	4	US-09-497-625A-14	Sequence 14, Appl
20	537	77.6	132	1	US-08-477-877B-91	Sequence 91, Appl
21	537	77.6	132	2	US-08-472-281A-91	Sequence 91, Appl
22	537	77.6	132	2	US-08-477-989B-91	Sequence 91, Appl
23	533	77.0	112	4	US-09-809-739-17	Sequence 17, Appl
24	533	77.0	112	4	US-09-840-459-15	Sequence 15, Appl
25	533	77.0	112	4	US-09-497-625A-15	Sequence 15, Appl
26	530	76.6	112	4	US-09-809-739-15	Sequence 15, Appl
27	530	76.6	112	4	US-09-840-459-13	Sequence 13, Appl
28	530	76.6	112	4	US-09-497-625A-13	Sequence 13, Appl
29	527	76.2	114	4	US-09-840-459-106	Sequence 106, App
30	527	76.2	114	4	US-09-497-625A-106	Sequence 106, App
31	525	75.9	112	4	US-09-809-739-18	Sequence 18, Appl
32	525	75.9	112	4	US-09-840-459-107	Sequence 107, App
33	520	75.1	112	4	US-09-809-739-14	Sequence 14, Appl
34	520	75.1	112	4	US-09-840-459-12	Sequence 12, Appl
35	520	75.1	112	4	US-09-497-625A-12	Sequence 12, Appl
36	518	74.9	132	1	US-08-477-877B-84	Sequence 84, Appl
37	518	74.9	132	2	US-08-472-281A-84	Sequence 84, Appl
38	518	74.9	132	2	US-08-477-989B-84	Sequence 84, Appl
39	515	74.4	100	4	US-09-840-459-22	Sequence 22, Appl
40	515	74.4	100	4	US-09-497-625A-22	Sequence 22, Appl
41	515	74.4	135	1	US-08-259-372A-12	Sequence 12, Appl
42	515	74.4	135	1	US-08-468-671-12	Sequence 12, Appl
43	512	74.0	112	3	US-09-184-658-49	Sequence 49, Appl
44	512	74.0	112	4	US-09-504-262D-49	Sequence 49, Appl
45	508	73.4	289	3	US-09-184-658-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-09-647-468-163

```

; Sequence 163, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-163

Query Match 93.8%; Score 649; DB 4; Length 131;
Best Local Similarity 93.9%; Pred. No. 5.4e-55;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY	2	MSPAQFLFLVLWIRETNGYVVTQPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL	61
		: :	
Db	1	MSPAQFLFLVLWIREINGDVVLTQPLTLSVTIGQPASVSKSSQSLLSDGKTYLNWL	60
QY	62	LQRPGQSPKRLLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR	121
		: :	
Db	61	LQRPGQSPKRLLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD	120
QY	122	TFGGGTKLEIK	132
Db	121	TFGGGTKLEIK	131

RESULT 2

US-09-647-468-164
; Sequence 164, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amoino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164

Query Match 93.4%; Score 646; DB 4; Length 131;
 Best Local Similarity 93.1%; Pred. No. 1e-54;
 Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

 Qy 2 MSPAQFLFLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
 |||||||:|||:|||||||||:|||||||||:|||||||||:|||||||||
 Db 1 MSPAQFLFLVLWIRDINGDVVLQTPLTLSVTIGQPASVSCKSSQSLLSDGKTYLNWL 60

 Qy 62 LQRPQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCQWQGTHFPR 121
 |||||||:|||||||||:|||||||||:|||||:|||||
 Db 61 LQRPQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCQDTHFPD 120

 Qy 122 TFGGGTKLEIK 132
 |||||||
 Db 121 TFGGGTKLEIK 131

RESULT 3

US-09-840-459-102

; Sequence 102, Application US/09840459

; Patent No. 6696550

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855.1052-012
 ; CURRENT APPLICATION NUMBER: US/09/840,459
 ; CURRENT FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: PCT/US01/03537
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/497,625
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 102
 ; LENGTH: 142
 ; TYPE: PRT
 ; ORGANISM: Mus musculus

US-09-840-459-102

Query Match 87.6%; Score 606; DB 4; Length 142;
 Best Local Similarity 93.5%; Pred. No. 7.8e-51;
 Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

 Qy 10 LLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLQRPQSP 69
 |||||||:|||||||||:|||||||||:|||||||||:|||||||||
 Db 7 LLVLWIRETIGDVVMQTPLTLSVTGHPASISCKSSQSLLSDGKTFLNWLLQRPQSP 66

; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELER, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
; TITLE OF INVENTION: BINDING COMPONENTS
; FILE REFERENCE: MXI-099CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4

Query Match 81.2%; Score 562; DB 4; Length 353;
Best Local Similarity 94.6%; Pred. No. 3.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
Db 177 VVMTQTPLTLSITIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPTRLIYLVSKLDS 236

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 237 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFQTFGGGTKEIK 287

RESULT 6

US-09-809-739-11

; Sequence 11, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

;
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
;
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
;
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
;
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
;
; OTHER INFORMATION: Mouse
US-09-809-739-11

Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 VVMTQTPLTLSVTVGHQPASISCKSSQSLSDGKTFLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKEIK 112

RESULT 7

US-09-840-459-9

;
; Sequence 9, Application US/09840459
;
; Patent No. 6696550
;
; GENERAL INFORMATION:
;
; APPLICANT: LaRosa, Gregory J.
;
; APPLICANT: Horvath, Christopher
;
; APPLICANT: Newman, Walter
;
; APPLICANT: Jones, S. Tarran
;
; APPLICANT: O'Brien, Siobhan H.
;
; APPLICANT: O'Keefe, Theresa
;
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
;
; TITLE OF INVENTION: METHODS OF USE THEREFOR
;
; FILE REFERENCE: 1855.1052-012
;
; CURRENT APPLICATION NUMBER: US/09/840,459
;
; CURRENT FILING DATE: 2001-02-02
;
; PRIOR APPLICATION NUMBER: PCT/US01/03537
;
; PRIOR FILING DATE: 2001-02-02
;
; PRIOR APPLICATION NUMBER: 09/497,625
;
; PRIOR FILING DATE: 2000-02-03
;
; PRIOR APPLICATION NUMBER: 09/359,193
;
; PRIOR FILING DATE: 1999-07-22
;
; PRIOR APPLICATION NUMBER: 09/121,781
;
; PRIOR FILING DATE: 1998-07-23
;
; NUMBER OF SEQ ID NOS: 107
;
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 9
;
; LENGTH: 112
;
; TYPE: PRT

; ORGANISM: *Mus musculus*
US-09-840-459-9

Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIK 112

RESULT 8

US-09-497-625A-9

; Sequence 9, Application US/09497625A

; Patent No. 6727349

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR

; FILE REFERENCE: 1855.1052-004

; CURRENT APPLICATION NUMBER: US/09/497,625A

; CURRENT FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 9

; LENGTH: 112

; TYPE: PRT

; ORGANISM: *Mus musculus*

US-09-497-625A-9

Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIK 112

RESULT 9

US-09-647-468-149

; Sequence 149, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-7

US-09-647-468-149

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
||:|||||||||||||:|||||||||||||||||||||||||

Db 2 VVLTQTPLTLSVTIGQPASVSKSSQSLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKRISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||||||||||:|||||:||||| ||||| |||||

Db 62 GVPDRFTGSGSGTDFTLKRISRVEAEDLGVYYCWQDTHFPDTFGGGTKLEIK 112

RESULT 10

US-09-647-468-150

; Sequence 150, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
||:|||||||||||||:|||||||||||||||||||||||||||||||||||||
Db 2 VVLTQTPLTLSVTIGQPASVSKSSQSLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||||||||||:|||||:||||| ||||| |||||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDTFGGGTKLEIK 112

RESULT 11

US-09-840-459-54

; Sequence 54, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-54

Query Match 80.3%; Score 556; DB 4; Length 112;
 Best Local Similarity 92.8%; Pred. No. 3.7e-46;
 Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

 Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLDS DGKTYLNWLLQRPGQSPKR LIYLVSKLDS 81
 : :||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2 IQLTQSPLTLSVTIGQPASISCKSSQSLDS DGKTYLNWLLQRPGQSPKR LIYLVSKLDS 61

 Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
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 Db 62 GVPDRFTGSGSGTDFTLKISRVEADDLGVYYCWQGTHFPQTFGGGTKLEIK 112

RESULT 12

US-09-497-625A-54

; Sequence 54, Application US/09497625A
 ; Patent No. 6727349
 ; GENERAL INFORMATION:
 ; APPLICANT: LaRosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855.1052-004
 ; CURRENT APPLICATION NUMBER: US/09/497,625A
 ; CURRENT FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 54
 ; LENGTH: 112
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-497-625A-54

Query Match 80.3%; Score 556; DB 4; Length 112;
 Best Local Similarity 92.8%; Pred. No. 3.7e-46;
 Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

 Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLDS DGKTYLNWLLQRPGQSPKR LIYLVSKLDS 81
 : :||:|||||||||||||||||||||||||||||||||||||||
 Db 2 IQLTQSPLTLSVTIGQPASISCKSSQSLDS DGKTYLNWLLQRPGQSPKR LIYLVSKLDS 61

 Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 ||||||||||||||||||:|||:|||:||||||||:|||||||||||
 Db 62 GVPDRFTGSGSGTDFTLKISRVEADDLGVYYCWQGTHFPQTFGGGTKLEIK 112

RESULT 13

US-08-678-194-6

; Sequence 6, Application US/08678194

Patent No. 5922845
GENERAL INFORMATION:
APPLICANT: Deo, Yashwant M.
APPLICANT: Graziano, Robert
APPLICANT: Keler, Tibor
TITLE OF INVENTION: Therapeutic Multispecific Compounds
TITLE OF INVENTION: Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"} Receptor Antibodi
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/678,194
FILING DATE: July 11, 1996
PRIOR APPLICATION DATA: No. 5922845e
APPLICATION NUMBER: US
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Beth A. Arnold
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-678-194-6

Query Match 79.2%; Score 548; DB 2; Length 112;
Best Local Similarity 91.0%; Pred. No. 2.2e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81

Pb 2 IOLTO SPLIT SITIGOPASI SCKSSO LIDSDGKTYL NWL IORPGOSPTRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132

Pb 62 GVPDR~~T~~GSGCTDE~~L~~KISRV~~A~~EDLGIY~~C~~WOGAHEPOTEGGGT~~K~~LEIK 112

RESULT 14

US-08-890-011-6

; Sequence 6, Application US/08890011
; Patent No. 6193966
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; TITLE OF INVENTION: Comprised of Anti-Fc
; TITLE OF INVENTION: {SYMBOL 97 \f "Symbol"} Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,011
; FILING DATE: July 9, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/678,194
; FILING DATE: July 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-064CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-011-6

Query Match 79.2%; Score 548; DB 3; Length 112;
Best Local Similarity 91.0%; Pred. No. 2.2e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
: : ||:||||:|||||||||||||||||||||||||||||||||||||| |||||||||
Db 2 IQLTQSPLTLSITIGQPASISCKSSQSLSDGKTYLNWLLQRPGQSPTRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
||||||||||||||||:||||||:|||||| ||||:|||||||||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

US-09-262-724-6

; Sequence 6, Application US/09262724

; Patent No. 6303755

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; Graziano, Robert

; Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"}

; Receptor Antibodies

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,724

; FILING DATE: 04-Mar-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194

; FILING DATE: July 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Beth A. Arnold

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MXI-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-262-724-6

Query Match 79.2%; Score 548; DB 3; Length 112;

Best Local Similarity 91.0%; Pred. No. 2.2e-45;

Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81

: :||:||||:||||||||||||||||||||||||||||||||||||||| |||||||

Db 2 IQLTQSPLTLSITIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPTRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGTHFPRTFGGGTKLEIK 132

|||||||||||||||||:|||||:|||||:||||| |||:|||||

Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

Search completed: December 13, 2004, 19:19:40
Job time : 28.3778 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:04:43 ; Search time 23.4667 Seconds
(without alignments)
541.219 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	678	98.0	132	2	C32513	Ig kappa chain pre
2	587	84.8	131	2	S31577	Ig kappa chain m
3	566	81.8	113	2	F30560	Ig kappa chain V r
4	554	80.1	112	2	A55491	proteolytic antibo
5	548	79.2	112	2	A36259	ig kappa chain V r
6	547	79.0	111	2	S20709	Ig kappa chain V r
7	536	77.5	112	2	PL0273	Ig kappa chain V r
8	516	74.6	133	2	S42611	HUNVK protein prec
9	515	74.4	101	2	A33730	Ig kappa chain V r
10	515	74.4	133	2	S23230	Ig kappa chain pre
11	513	74.1	142	2	S22902	Ig kappa chain V r
12	512	74.0	133	2	S40324	Ig kappa chain V r
13	508	73.4	133	1	K2HURP	Ig kappa chain pre

14	502.5	72.6	140	2	S22658	Ig kappa chain pre
15	496	71.7	133	1	A24452	Ig kappa chain pre
16	491	71.0	132	2	S40322	Ig kappa chain - h
17	485	70.1	103	2	PH1055	Ig light chain V r
18	476	68.8	91	2	S42186	Ig kappa chain V r
19	473	68.4	120	2	S42268	Ig kappa chain V r
20	473	68.4	120	2	S42267	Ig kappa chain V r
21	470	67.9	131	2	S09259	Ig kappa chain pre
22	466	67.3	103	2	PH1056	Ig light chain V r
23	463	66.9	126	2	S40312	Ig kappa chain - h
24	463	66.9	131	2	D29380	Ig kappa chain pre
25	462.5	66.8	131	2	S40355	Ig kappa chain - h
26	462	66.8	132	2	S26882	Ig kappa chain V r
27	461.5	66.7	114	2	S49572	Ig kappa chain pre
28	460	66.5	118	2	S40374	Ig kappa chain - h
29	458.5	66.3	114	2	B49002	Ig kappa chain V r
30	458	66.2	131	2	B34904	Ig kappa chain pre
31	458	66.2	136	2	S40357	Ig kappa chain V-J
32	456	65.9	112	2	A31807	Ig kappa chain V r
33	456	65.9	131	2	B39276	Ig light chain pre
34	455	65.8	132	2	PH0106	anti-digoxin trans
35	454	65.6	131	2	C34904	Ig kappa chain pre
36	452.5	65.4	134	2	S40376	Ig kappa chain - h
37	452	65.3	122	2	S40338	Ig kappa chain - h
38	451	65.2	128	2	S40373	Ig kappa chain - h
39	450.5	65.1	130	2	S40321	Ig kappa chain - h
40	450	65.0	131	2	D34904	Ig kappa chain pre
41	450	65.0	131	2	B30577	Ig kappa chain pre
42	448	64.7	131	2	G34903	Ig kappa chain pre
43	448	64.7	135	2	S40342	Ig kappa chain - h
44	447	64.6	131	2	B32513	Ig kappa chain pre
45	446	64.5	115	2	S38715	Ig kappa chain V r

ALIGNMENTS

RESULT 1

C32513

Ig kappa chain precursor V region (BXW14) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C;Accession: C32513

R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.;

Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.

J. Clin. Invest. 82, 852-860, 1988

A;Title: Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.

A;Reference number: A94689; MUID:88331394; PMID:3138286

A;Accession: C32513

A;Molecule type: DNA

A;Residues: 1-132 <KOF>

A;Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 678; DB 2; Length 132;
 Best Local Similarity 97.7%; Pred. No. 1.6e-51;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 ||||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
 ||||||||||||||||| ||||||||||||||| :|||||:|||||:|||||
 Db 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
 |||||||||||
 Db 121 RTFGGGTKLEIK 132

RESULT 2
 S31577
 Ig kappa chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C;Accession: S31577
 R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
 submitted to the EMBL Data Library, January 1993
 A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for
 two antidiotoxin monoclonals.
 A;Reference number: S31577
 A;Accession: S31577
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-131 <REC>
 A;Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 587; DB 2; Length 131;
 Best Local Similarity 86.3%; Pred. No. 1.1e-43;
 Matches 113; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
 ||||||||:|| |:| || ||||| |||||||:||||| ||||| |||||||
 Db 1 MSPAQFLFLLVLSIQEINGDVVMTQAPLTLGQPASISCKSSHSLLSIDGKTYLNWL 60

Qy 62 LQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWWQGTHFP 121
 |||||||||||||||||:|||||:|||||:|||||:|||||:||| | |||
 Db 61 LQRPQSPKRLIYLVSKLDGVPDRFSGSGSGTDFTLRISRVEAEDLGVYYCMQNTHFPY 120

Qy 122 TFGGGTKEIK 132
 ||||||||:|
 Db 121 TFGGGTKEIK 131

RESULT 3
 F30560

Ig kappa chain V region (28.4.10A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: F30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1->6)dextran.
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: F30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <MAT>
A;Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

RESULT 4

A55491
proteolytic antibody light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55491
R;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.;
Massey, R.J.; Paul, S.
J. Biol. Chem. 269, 32389-32393, 1994
A;Title: Molecular cloning of a proteolytic antibody light chain.
A;Reference number: A55491; MUID:95096089; PMID:7798238
A;Accession: A55491
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <GAO>
A;Cross-references: UNIPROT:Q8K0F8; GB:L34775
A;Note: authors translated the codon TAT for residue 37 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

```

Query Match          80.1%;  Score 554;  DB 2;  Length 112;
Best Local Similarity  94.6%;  Pred. No. 6.4e-41;
Matches 105;  Conservative 4;  Mismatches 2;  Indels 0;  Gaps 0;

Qy          22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81

```

Db ||||||| :||||| ||||||| :|||||
2 VVMTQTPLTLSVTIGQPASISCKSSQSLHDGKTYLIWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGYYCQGTHFPRTFGGGTKLEIK 132
 ||||| :||||| :||||| :|||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGYYCQGTHFPQTFGGGTKEIK 112

RESULT 5

A36259

ig kappa chain V region (TE34) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000
C;Accession: A36259
R;Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 29, 10032-10041, 1990
A;Title: NMR-derived model for a peptide-antibody complex.
A;Reference number: A36259; MUID:91104915; PMID:2271636
A;Accession: A36259
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <ZIL>
A;Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482;
GB:M30483
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 548; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.1e-40;
Matches 105; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
 ||||| :||||| :|||||
Db 2 VVMIQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGYYCQGTHFPRTFGGGTKLEIK 132
 ||||| :||||| :|||||
Db 62 GVPTRFTGSGSGTDFTLKISRVEAEDGGVYYCQGTHFPWTFGGGTKLEIK 112

RESULT 6

S20709

Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20709
R;Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osborn, N.J.; Glennie, M.J.; Richards, N.G.; Robinson, J.A.
submitted to the EMBL Data Library, April 1992
A;Description: Binding specificity and variable region sequences of two monoclonal antibodies that recognise a beta-turn forming peptide containing alpha-methylproline.
A;Reference number: S20706
A;Accession: S20709
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-111 <BRE>
A;Cross-references: EMBL:Z11917; .NID:g52655; PIDN:CAA77975.1; PID:g52656
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 547; DB 2; Length 111;
Best Local Similarity 92.7%; Pred. No. 2.5e-40;
Matches 102; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
: :||:||||||||||||||||||||| :|||||||||||||||||
Db 2 IQLTQSPPLTLSVTIGQPASISCKSSQSLLHSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEI 131
|||||||||||||||||:|||||:|||||:|||||:|||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEI 111

RESULT 7

PL0273

Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: PL0273

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0273

A;Molecule type: mRNA

A;Residues: 1-112 <SHL>

A;Cross-references: UNIPROT:Q8K0F8

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-95/Domain: immunoglobulin homology <IMM>

F;24-39/Region: complementarity-determining 1

F;40-54/Region: framework 2

F;55-61/Region: complementarity-determining 2

F;62-93/Region: framework 3

F;94-102/Region: complementarity-determining 3

F;103-112/Region: framework 4

Query Match 77.5%; Score 536; DB 2; Length 112;
Best Local Similarity 93.7%; Pred. No. 2.3e-39;
Matches 104; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
||||||||||||||||| :|||||||||||||||||
Db 2 VVMTQTPLTLSVTIGQPASISCKSSQSLLYRNGKTYLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||||||||||:|||||:||| ||||| |||||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPWTGGGTKLEIK 112

RESULT 8

S42611

HUNVK protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S42611

R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.

J. Neuroimmunol. 36, 29-39, 1992

A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regions of two IgM, monoclonal, anti-myelin associated glycoprotein antibodies.

A;Reference number: S42610; MUID:92138794; PMID:1370957

A;Accession: S42611

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <SPA>

A;Cross-references: EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PID:g433890

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 516; DB 2; Length 133;
Best Local Similarity 74.0%; Pred. No. 1.4e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60
| ||| | ||:||: ::| |||||:||:| ||:|||||||:|||||: ||| |||||

Db 1 MRLPAQLLGLMLWVPGSSGDVVMQTQSPSLPVTLGQPASISCRSSQSLVFSDGNTYLNW 60

Qy 61 LLQRPGQSPKRLLIYLVSKLDGVPDRFTGSGSGTDFTLKISREREAEDLGLYYCWQGTHFP 120
|||||||:|||| ||| |||||||:|||||||||:|||||:||| ||| ||| :|

Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQGAHWP 120

Qy 121 RTFGGGTKLEI 131

|||||||:||

Db 121 LTFGGGTTKVEI 131

RESULT 9

A33730

Ig kappa chain V region (1.60) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000

C;Accession: A33730

R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unlike genes encoding heavy chains, use variable gene segments dispersed throughout the locus.

A;Reference number: A33730; MUID:89367325; PMID:2505260

A;Accession: A33730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <LAW>

A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110

A;Note: the authors translated the codon CGC for residue 51 as Leu, and TTG for residue 88 as Phe
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 101;
Best Local Similarity 98.0%; Pred. No. 1.3e-37;
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 100

RESULT 10
S23230
Ig kappa chain precursor V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23230
R;Kennedy, M.A.
J. Exp. Med. 173, 1033-1036, 1991
A;Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light chain V genes in a human B lymphoblastoid cell line.
A;Reference number: S23230; MUID:91178438; PMID:1840606
A;Accession: S23230
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <KEN>
A;Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 133;
Best Local Similarity 74.2%; Pred. No. 1.7e-37;
Matches 98; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1..MMSPAQFLFLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db 1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPSLPVTLGQPAISCRSSQSLVYSDGNTHLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
Db 61 FQQRPQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 YTFGQGKLEIK 132

RESULT 11

S22902

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S22902

R;Chastagner, P.; Theze, J.; Zouali, M.

Gene 101, 305-306, 1991

A;Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region using the polymerase chain reaction and degenerate primers.

A;Reference number: S22902; MUID:91276289; PMID:1905262

A;Accession: S22902

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-142 <CHA>

A;Cross-references: EMBL:X56510

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-126/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 513; DB 2; Length 142;
Best Local Similarity 74.0%; Pred. No. 2.7e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTQPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| ||| | ||:||: ::| |||||:||:| ||:|||||||:||||:| ||| |||||

Db 12 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 71

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKRISRVEAEDLGLYYCWQGTHFP 120
| |||||:||| ||| ||| |||||:||||| ||| |||:|||:||| |||:|

Db 72 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKRISRVEAEDVGVYYCMQGTHWP 131

Qy 121 RTFGGGTKLEI 131
| ||| ||:|||

Db 132 FTFGQGTRLEI 142

RESULT 12

S40324

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C;Accession: S40324

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40324

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-133 <KLE>

A;Cross-references: UNIPROT:Q8TC0; EMBL:X72434

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-112/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 512; DB 2; Length 133;
 Best Local Similarity 74.4%; Pred. No. 3.1e-37;
 Matches 96; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

 QY 4 PAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQ 63
 ||| | ||:||: ::| ||:||:||:| ||:|||||||:| |||: ||||| ||| |
 Db 1 PAQLLGLLMLWVPGSSGVDVLTQSPSLPVTLGQPASISCRSDQSLVYSDGKTYLNWYQQ 60

 QY 64 RPGQSPKRLLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTF 123
 |||||:||| ||| ||| |||:|||:|||:|||:|||:|||:|||:|||:|||:|||
 Db 61 RPGQSPRRLIYKVSNRDGSVPDRFTGSGSGTDFTLIEISRVEAEDVGVYYCMQGTHWPPTF 120

 QY 124 GGGTKLEIK 132
 | |||:|||
 Db 121 GQGTKVEIK 129

RESULT 13

K2HURP

Ig kappa chain precursor V-II region (RPMI) - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A01890
 R;Klobbeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
 Nucleic Acids Res. 13, 6499-6513, 1985
 A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
 A;Reference number: A93588; MUID:86041852; PMID:2997711
 A;Accession: A01890
 A;Molecule type: DNA
 A;Residues: 1-133 <KLO>
 A;Cross-references: UNIPROT:P06310
 A;Note: the sequence was determined from the differentiated gene
 C;Genetics:
 A;Gene: GDB:IGKV2
 A;Cross-references: GDB:136265
 A;Map position: 2p12-2p12
 A;Introns: 17/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
 F;21-43/Region: framework 1
 F;36-115/Domain: immunoglobulin homology <IMM>
 F;44-59/Region: complementarity-determining 1
 F;60-74/Region: framework 2
 F;75-81/Region: complementarity-determining 2
 F;82-113/Region: framework 3
 F;114-122/Region: complementarity-determining 3
 F;123-133/Region: framework 4
 F;43-113/Disulfide bonds: #status predicted

Query Match 73.4%; Score 508; DB 1; Length 133;
 Best Local Similarity 73.5%; Pred. No. 6.9e-37;

Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 | ||| | ||:||: ::| |||||:||:| ||:|||||||:|||||: ||| |||||

Db 1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCQGTHFP 120
 |||||||:|||| ||| |||||||:|||||||||:|||||:|||:|||:|||:

Db 61 FQQRPGQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120

Qy 121 RTFGGGTKLEIK 132
 ||| |||:|||

Db 121 WTFGQGKVEIK 132

RESULT 14

S22658

Ig kappa chain precursor V region (0-81VL) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004

C;Accession: S22658

R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22658

A;Molecule type: mRNA

A;Residues: 1-140 <HIR>

A;Cross-references: UNIPROT:Q8TC0; EMBL:X59135

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.6%; Score 502.5; DB 2; Length 140;
 Best Local Similarity 73.7%; Pred. No. 2.2e-36;
 Matches 98; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 | ||| | ||:||: ::| |||||:||:| ||:|||||||:|||||: ||| |||||

Db 1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCQGTHF- 119
 |||||||:|||| ||| |||||||:|||:|||||||:|||||:|||:||| + ||:

Db 61 FQQRPGQSPRRLIYRVSNRDGSVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQHTHWS 120

Qy 120 PRTFGGGTKLEIK 132

 | ||| ||:|||

Db 121 PITFGQGTRLEIK 133

RESULT 15

A24452

Ig kappa chain precursor V-II region (RPMI 6410) - human

C;Species: Homo sapiens (man)

C;Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C;Accession: A24452
R;Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A;Reference number: A24452; MUID:86232631; PMID:3086847
A;Accession: A24452
A;Molecule type: DNA
A;Residues: 1-133 <WEI>
A;Cross-references: GB:M36859; NID:g185932; PIDN:AAA58920.1; PID:g185933
A;Note: this sequence was determined from the differentiated gene
C;Genetics:
A;Gene: GDB:IGKV2
A;Cross-references: GDB:136265
A;Map position: 2p12-2p12
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <IMM>
F;43-113/Disulfide bonds: #status predicted

Query Match 71.7%; Score 496; DB 1; Length 133;
Best Local Similarity 72.7%; Pred. No. 7.4e-36;
Matches 96; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY	1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
	: :: : : : : :
Db	1 MRLPAQLLGLLRLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDRNTYLNW 60
QY	61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
	: : : : : : :
Db	61 FQQRPGQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120
QY	121 RTFGGGTKLEIK 132
	:
Db	121 WTFGQGTKVEIK 132

Search completed: December 13, 2004, 19:18:39
Job time : 25.4667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:17:53 ; Search time 94.8444 Seconds
(without alignments)
497.104 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLLVIWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	692	100.0	132	14	US-10-010-942B-2	Sequence 2, Appli
2	692	100.0	132	15	US-10-388-389-2	Sequence 2, Appli
3	692	100.0	132	16	US-10-703-713-2	Sequence 2, Appli
4	692	100.0	132	16	US-10-704-070-2	Sequence 2, Appli
5	650	93.9	135	9	US-09-881-823-10	Sequence 10, Appli
6	649	93.8	131	15	US-10-462-062-163	Sequence 163, App
7	646	93.4	131	15	US-10-462-062-164	Sequence 164, App
8	640	92.5	132	14	US-10-010-942B-5	Sequence 5, Appli
9	640	92.5	132	15	US-10-388-389-5	Sequence 5, Appli
10	640	92.5	132	16	US-10-703-713-5	Sequence 5, Appli
11	640	92.5	132	16	US-10-704-070-5	Sequence 5, Appli
12	636	91.9	132	13	US-10-006-773-11	Sequence 11, Appli
13	630	91.0	132	14	US-10-010-942B-11	Sequence 11, Appli
14	630	91.0	132	15	US-10-388-389-11	Sequence 11, Appli
15	630	91.0	132	16	US-10-703-713-11	Sequence 11, Appli
16	630	91.0	132	16	US-10-704-070-11	Sequence 11, Appli
17	606	87.6	142	9	US-09-840-459-102	Sequence 102, App
18	606	87.6	142	16	US-10-766-773-102	Sequence 102, App
19	606	87.6	142	16	US-10-766-610-102	Sequence 102, App
20	606	87.6	142	16	US-10-733-563-102	Sequence 102, App
21	562	81.2	353	10	US-09-203-958A-4	Sequence 4, Appli
22	560	80.9	112	9	US-09-835-087-1	Sequence 1, Appli
23	560	80.9	112	9	US-09-809-739-11	Sequence 11, Appli
24	560	80.9	112	9	US-09-840-459-9	Sequence 9, Appli
25	560	80.9	112	16	US-10-766-773-9	Sequence 9, Appli
26	560	80.9	112	16	US-10-766-610-9	Sequence 9, Appli
27	560	80.9	112	16	US-10-733-563-9	Sequence 9, Appli
28	560	80.9	122	15	US-10-272-899A-86	Sequence 86, Appli
29	560	80.9	130	15	US-10-272-899A-88	Sequence 88, Appli
30	559	80.8	112	15	US-10-462-062-149	Sequence 149, App
31	559	80.8	112	15	US-10-462-062-150	Sequence 150, App
32	556	80.3	112	9	US-09-840-459-54	Sequence 54, Appli
33	556	80.3	112	16	US-10-766-773-54	Sequence 54, Appli
34	556	80.3	112	16	US-10-766-610-54	Sequence 54, Appli
35	556	80.3	112	16	US-10-733-563-54	Sequence 54, Appli
36	551	79.6	500	14	US-10-168-809-22	Sequence 22, Appli
37	548	79.2	112	9	US-09-772-120-6	Sequence 6, Appli
38	548	79.2	535	9	US-09-968-851-38	Sequence 38, Appli
39	547	79.0	162	14	US-10-410-907A-30	Sequence 30, Appli
40	546	78.9	112	14	US-10-323-903-1	Sequence 1, Appli
41	538	77.7	112	9	US-09-835-087-5	Sequence 5, Appli
42	538	77.7	112	9	US-09-809-739-16	Sequence 16, Appli
43	538	77.7	112	9	US-09-840-459-14	Sequence 14, Appli
44	538	77.7	112	16	US-10-766-773-14	Sequence 14, Appli
45	538	77.7	112	16	US-10-766-610-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
 US-10-010-942B-2
 ; Sequence 2, Application US/10010942B
 ; Publication No. US20030165496A1

; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2

Query Match 100.0%; Score 692; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MMSPAQFLLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRIAEDLGLYYCWQGTHFP 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRIAEDLGLYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
||| ||| ||| |||
Db 121 RTFGGGTKLEIK 132

RESULT 2

US-10-388-389-2

; Sequence 2, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-388-389-2

Query Match 100.0%; Score 692; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
|||
Db 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
|||
Db 61 LLQRPQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
|||
Db 121 RTFGGGTKLEIK 132

RESULT 3

US-10-703-713-2

; Sequence 2, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-703-713-2

Query Match 100.0%; Score 692; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
||||||||||||||||||||||||||||||||||||||||

Db 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
||||||||||||

Db 121 RTFGGGTKLEIK 132

RESULT 4

US-10-704-070-2

; Sequence 2, Application US/10704070

; Publication No. US20040171816A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Guriq

; APPLICANT: Salданха, Jose

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

; FILE REFERENCE: ELN-002CP

; CURRENT APPLICATION NUMBER: US/10/704,070

; CURRENT FILING DATE: 2003-11-07

; PRIOR APPLICATION NUMBER: 10/388,389

; PRIOR FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 10/010,942

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: US 60/251,892

; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 132

; TYPE: PRT

; ORGANISM: *Mus musculus*

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(20)

US-10-704-070-2

Query Match 100.0%; Score 692; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||||||||||||||||||||||||||||||||||||

Db 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
||||||||||||||||||||||||||||||||||||

Db 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
Qy 121 RTFGGGTKLEIK 132
Db 121 RTFGGGTKLEIK 132

RESULT 5
US-09-881-823-10
; Sequence 10, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-10

Query Match 93.9%; Score 650; DB 9; Length 135;
Best Local Similarity 93.2%; Pred. No. 4.7e-53;
Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNW 60
Db 1 MMSPAQFLFLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLDRDGRTYLSW 60
Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
Db 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 120
Qy 121 RTFGGGTKLEIK 132
Db 121 LTFGAGTKLEIK 132

RESULT 6
US-10-462-062-163
; Sequence 163, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-7
US-10-462-062-163

Query Match 93.8%; Score 649; DB 15; Length 131;
Best Local Similarity 93.9%; Pred. No. 5.7e-53;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
Db 1 MSPAQFLFLLVLWIREINGDVVLQTPLTLSVTIGQPASVSKSSQSLLSDGKTYLNWL 60

Qy 62 LQRPGQSPKRRIYLVSKLDGVPDRFTGSGSGTDFTLKRISRVEAEDLGLYYCQGTHFPR 121
Db 61 LQRPGQSPKRRIYLVSKLDGVPDRFTGSGSGTDFTLKRISRVEAEDLGVYYCQDTHFPD 120

Qy 122 TFGGGTKLEIK 132
Db 121 TFGGGTKLEIK 131

RESULT 7
US-10-462-062-164
; Sequence 164, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164

; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-8
US-10-462-062-164

Query Match 93.4%; Score 646; DB 15; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.1e-52;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWL 61
|||:|||||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSPAQFLFLLVLWIRDINGDVVLTQTPLTLSVTIGQPASVSCKSSQSLSDGKTYLNWL 60

Qy 62 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWDTHFPD 120

Qy 122 TFGGGTKLEIK 132
|||:|||||:
Db 121 TFGGGTKLEIK 131

RESULT 8
US-10-010-942B-5
; Sequence 5, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-5

Query Match 92.5%; Score 640; DB 14; Length 132;
Best Local Similarity 90.2%; Pred. No. 4e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSVTIGQPASISCKSSQSLDSDGKTYLNW 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 MMSPAQFLFLLVLWIRETNGYVVMTQSPLSLPVTPGEPASISCKSSQSLDSDGKTYLNW 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
 ||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120
 ||||:||||:|||||:
 Qy 121 RTFGGGTKLEIK 132
 |||| |||:
 Db 121 RTFGQGTTKVEIK 132

RESULT 9

US-10-388-389-5

; Sequence 5, Application US/10388389
 ; Publication No. US20040087777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basi, Guriq
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
 ; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
 ; FILE REFERENCE: ELN-002CP
 ; CURRENT APPLICATION NUMBER: US/10/388,389
 ; CURRENT FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: US 10/010,942
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: US 60/251,892
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(20)
 ; OTHER INFORMATION: humanized 3D6 light chain variable region

US-10-388-389-5

Query Match 92.5%; Score 640; DB 15; Length 132;
 Best Local Similarity 90.2%; Pred. No. 4e-52;
 Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSVTIGQPASISCKSSQSLDSDGKTYLNW 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 MMSPAQFLFLLVLWIRETNGYVVMTQSPLSLPVTPGEPASISCKSSQSLDSDGKTYLNW 60
 |||||||:|||||:|||||:|||||:|||||:
 Qy 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
 ||||:||||:|||||:|||||:|||||:|||||:
 Db 61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120
 ||||:||||:
 Qy 121 RTFGGGTKLEIK 132
 |||| |||:

Db 121 RTFGQGTKVEIK 132

RESULT 10
US-10-703-713-5
; Sequence 5, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-703-713-5

Query Match 92.5%; Score 640; DB 16; Length 132;
Best Local Similarity 90.2%; Pred. No. 4e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNW 60
Db 1 MMSPAQFLFLVLWIRETNGYVVMQTQSPSLPVTGEPASISCKSSQSLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDGLYYCWQGTHFP 120
Db 61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 RTFGQGTKVEIK 132

RESULT 11
US-10-704-070-5
; Sequence 5, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq

;

APPLICANT: Saldanha, Jose

;

APPLICANT: Yednock, Ted

;

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

;

TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

;

FILE REFERENCE: ELN-002CP

;

CURRENT APPLICATION NUMBER: US/10/704,070

;

CURRENT FILING DATE: 2003-11-07

;

PRIOR APPLICATION NUMBER: 10/388,389

;

PRIOR FILING DATE: 2003-03-12

;

PRIOR APPLICATION NUMBER: US 10/010,942

;

PRIOR FILING DATE: 2001-12-06

;

PRIOR APPLICATION NUMBER: US 60/251,892

;

PRIOR FILING DATE: 2000-12-06

;

NUMBER OF SEQ ID NOS: 63

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 5

;

LENGTH: 132

;

TYPE: PRT

;

ORGANISM: Artificial Sequence

;

FEATURE:

;

NAME/KEY: SIGNAL

;

LOCATION: (1)...(20)

;

OTHER INFORMATION: humanized 3D6 light chain variable region

US-10-704-070-5

US-10-704-070-5

RESULT 12

US-10-006-773-11

; Sequence 11, Application US/10006773

; Publication No. US20020132983A1

GENERAL INFORMATION:

; APPLICANT: Junghans, Richard P.

; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against

Tumor Antigens

; FILE REFERENCE: 003

; CURRENT APPLICATION NUMBER: US/10/006,773

; CURRENT FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 60/250,089

; PRIOR FILING DATE: 2000-11-30

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-11

Query Match 91.9%; Score 636; DB 13; Length 132;
Best Local Similarity 93.9%; Pred. No. 9.4e-52;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
|||||||||||||:|||||||||||||||||:|||||||||
Db 1 MSPAQFLFLLVLWIQETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWL 60

Qy 62 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR 121
|||||||||||||||||||||||||||||:|||||:|||||
Db 61 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPH 120

Qy 122 TFGGGTKLEIK 132
|||||||||||
Db 121 TFGGGTKLEIK 131

RESULT 13

US-10-010-942B-11

; Sequence 11, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-11

Query Match 91.0%; Score 630; DB 14; Length 132;
Best Local Similarity 89.4%; Pred. No. 3.4e-51;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
|||||||||||||||||:|||||:|||:|||||||||||||||||
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTGEPASISCKSSQSLLSDGKTYLNW 60

```

Qy      61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
       ||||:||||:||||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db      61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy      121 RTFGGGTKLEIK 132
       |||| |||:|||
Db      121 RTFGQGTTKVEIK 132

```

RESULT 14

US-10-388-389-11

; Sequence 11, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region

US-10-388-389-11

Query Match 91.0%; Score 630; DB 15; Length 132;
Best Local Similarity 89.4%; Pred. No. 3.4e-51;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

```

Qy      1 MMSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
       ||||||||||||||| ||||:||:| || |:||||||||||||||||| ||||:||:||||:|||
Db      1 MMSPAQFLFLVLWIRETNGDVVMTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

Qy      61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
       ||||:||||:||||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db      61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy      121 RTFGGGTKLEIK 132
       |||| |||:|||
Db      121 RTFGQGTTKVEIK 132

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RESULT 15

US-10-703-713-11
; Sequence 11, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region

US-10-703-713-11

Query Match 91.0%; Score 630; DB 16; Length 132;
Best Local Similarity 89.4%; Pred. No. 3.4e-51;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNW 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

QY 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

QY 121 RTFGGGTKLEIK 132
||||| |||:|||
Db 121 RTFGQGTTKVEIK 132

Search completed: December 13, 2004, 19:34:49
Job time : 95.8444 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 18:50:06 ; Search time 125.644 Seconds
(without alignments)
604.479 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	611	88.3	148	2	Q8K122	Q8k122 mus musculu
2	583	84.2	239	2	Q8K0F8	Q8k0f8 mus musculu
3	511	73.8	239	2	Q8TCDO	Q8tcd0 homo sapien
4	508	73.4	133	1	KV2F HUMAN	P06310 homo sapien
5	471	68.1	239	2	Q6P491	Q6p491 homo sapien
6	471	68.1	239	2	Q8NEK0	Q8nek0 homo sapien
7	471	68.1	239	2	AAH63599	Aah63599 homo sapi
8	460	66.5	238	2	Q99M37	Q99m37 mus musculu
9	459	66.3	238	2	Q8VCI6	Q8vci6 mus musculu
10	453	65.5	239	2	Q8VC55	Q8vc55 mus musculu
11	448	64.7	239	2	BAC04905	Bac04905 homo sapi
12	444.5	64.2	114	2	Q9UL80	Q9ul80 homo sapien
13	441.5	63.8	240	2	Q6PIH6	Q6pih6 homo sapien
14	441.5	63.8	240	2	AAH34142	Aah34142 homo sapi
15	436	63.0	114	2	AAR11017	Aar11017 mus muscu

16	434	62.7	113	1	KV2G_MOUSE	P01631	mus musculu
17	417	60.3	117	1	KV2E_HUMAN	P06309	homo sapien
18	415	60.0	113	1	KV2D_HUMAN	P01617	homo sapien
19	414.5	59.9	115	1	KV2A_HUMAN	P01614	homo sapien
20	414	59.8	113	1	KV2B_HUMAN	P01615	homo sapien
21	411	59.4	105	2	AAR11074	Aar11074	mus muscu
22	408.5	59.0	104	2	AAR11056	Aar11056	mus muscu
23	406	58.7	104	2	AAR11064	Aar11064	mus muscu
24	405	58.5	104	2	AAR11024	Aar11024	mus muscu
25	398	57.5	104	2	Q9JL82	Q9jl82	mus musculu
26	398	57.5	109	2	AAR10990	Aar10990	mus muscu
27	397	57.4	104	2	AAR11063	Aar11063	mus muscu
28	394	56.9	102	2	AAR11040	Aar11040	mus muscu
29	389.5	56.3	112	1	KV2C_HUMAN	P01616	homo sapien
30	388	56.1	113	1	KV2F_MOUSE	P01630	mus musculu
31	386	55.8	129	1	KV3L_HUMAN	P18135	homo sapien
32	381	55.1	112	2	Q6LEM8	Q6lem8	mus musculu
33	381	55.1	112	2	BAD00151	Bad00151	mus muscu
34	380.5	55.0	134	1	KV4C_HUMAN	P06314	homo sapien
35	380	54.9	113	1	KV2E_MOUSE	P03976	mus musculu
36	377.5	54.6	236	2	Q6PIL8	Q6pil8	homo sapien
37	377.5	54.6	236	2	AAH32451	Aah32451	homo sapien
38	376	54.3	235	2	Q6GMV9	Q6gmv9	homo sapien
39	374	54.0	112	1	KV2D_MOUSE	P01629	mus musculu
40	374	54.0	120	1	KV2B_MOUSE	P01627	mus musculu
41	373.5	54.0	131	1	KV3I_MOUSE	P01661	mus musculu
42	373	53.9	113	1	KV2C_MOUSE	P01628	mus musculu
43	373	53.9	129	1	KV3M_HUMAN	P18136	homo sapien
44	373	53.9	133	1	KV4B_HUMAN	P06313	homo sapien
45	369.5	53.4	240	2	Q6PJB5	Q6pjb5	homo sapien

ALIGNMENTS

RESULT 1

Q8K122

ID Q8K122 PRELIMINARY; PRT; 148 AA.
 AC Q8K122;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC028925; AAH28925.1; -.
 DR HSSP; Q8K0F8; 1KN2.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

 Query Match 88.3%; Score 611; DB 2; Length 148;
 Best Local Similarity 97.5%; Pred. No. 3.8e-51;
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 MSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 60

 Qy 62 LQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| :|||||:|||||:|||||
 Db 61 LQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 119

RESULT 2

Q8K0F8

ID Q8K0F8 PRELIMINARY; PRT; 239 AA.
 AC Q8K0F8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N;

RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC031498; AAH31498.1; -.
DR PIR; A33933; A33933.
DR PIR; A55491; A55491.
DR PIR; PH1055; PH1055.
DR PIR; PL0273; PL0273.
DR PDB; 1KN2; X-ray; L=21-239.
DR PDB; 1KN4; X-ray; L=21-239.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26367 MW; D7BE84398AA341F0 CRC64;

Query Match 84.2%; Score 583; DB 2; Length 239;
Best Local Similarity 87.1%; Pred. No. 3.4e-48;
Matches 115; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy	1	MMSPAQLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSL	LDSDGKTYLNW	60
		:	:	
Db	1	MMSPAQLFLLVLSTQEINGDVVMQTPLTLSVTIGQPASISCKSSOSL	FYTNGKMYLSW	60

RESULT 3

Q8TCDO0 PRELIMINARY; PRT; 239 AA.
ID Q8TCDO0;
AC Q8TCDO0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.

DR HSSP; P01834; 1I7Z.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

 Query Match 73.8%; Score 511; DB 2; Length 239;
 Best Local Similarity 72.7%; Pred. No. 3.2e-41;
 Matches 96; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

 Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNW 60
 | ||| | ||::|: ::| | ||||:||:| ||:||||||:|:||:| ||| | |||||
 Db 1 MRLPAQLLGLLMLWVPGSSGDIVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNW 60

 Qy 61 LLQRPGQSPKRRIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
 |||||||:|||| ||| ||||||||:|||||||:|:||||:|:| ||||:|
 Db 61 FQQRPGQSPRRIYKVSNRDGSVPDRFSGSGSGTDFTLKIRVEAEDVGVYFCMQGTHWP 120

 Qy 121 RTFGGGTKLEIK 132
 ||| |||||||
 Db 121 STFGQGKLEIK 132

RESULT 4

KV2F_HUMAN

ID KV2F_HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region RPMI 6410 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041852; PubMed=2997711;
 RA Klobbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 III.";
 RL Nucleic Acids Res. 13:6499-6513(1985).
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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; Z00020; CAA77315.1; -.
 DR PIR; A01890; K2HURP.
 DR HSSP; Q99M37; 1I9I.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 59 Complementarity-determining-1.
 FT DOMAIN 60 74 Framework-2.
 FT DOMAIN 75 81 Complementarity-determining-2.
 FT DOMAIN 82 113 Framework-3.
 FT DOMAIN 114 122 Complementarity-determining-3.
 FT DOMAIN 123 132 Framework-4.
 FT DISULFID 43 113 By similarity.
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 73.4%; Score 508; DB 1; Length 133;
 Best Local Similarity 73.5%; Pred. No. 3.2e-41;
 Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNW 60
 | ||| | ||:||: ::| |||||:|||:| ||:|||||||:|||||: ||| |||||
 Db 1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
 |||||||:|||| ||| |||||||:||||| |||||||:|||||:|:||| ||||:
 Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDFSGSGSGTDFTLKISRVEAEVGVYYCMQGTHWS 120

Qy 121 RTFGGGTKLEIK 132
 ||| |||:|||
 Db 121 WTFGQGTTKVEIK 132

RESULT 5

Q6P491

ID Q6P491 PRELIMINARY; PRT; 239 AA.
 AC Q6P491;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;
Best Local Similarity 68.8%; Pred. No. 2.4e-37;
Matches 88; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

QY 5 AQFLFLLVWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQR 64
|| | ||:||: ::| :|||||||: ||:|||||||:||:||| |:| |||:|| ||
Db 5 AQLLGLLMLWVPGSSGDIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQR 64
QY 65 PGQSPKRLLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFG 124
|| | : ||| :| |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 65 PGQPPRLLIYKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVSHFPRTFG 124
QY 125 GGTKLEIK 132
||:|||

RESULT 6

Q8NEKO

ID Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; 1I7Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

 Query Match 68.1%; Score 471; DB 2; Length 239;
 Best Local Similarity 68.2%; Pred. No. 2.4e-37;
 Matches 90; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

 QY 1 MMSPAQFLFLLVWIRETNGYVVMQTPLTISVTIGQPASISCKSSQSLDSDGKTYLNW 60
 | ||| | ||:|: ::| :|||:||:| || |:|||||:|||||| | ||| ||:|
 Db 1 MRLPAQLLGMLWVSGSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLHSDGNYLDW 60

 Qy 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
 ||:|||||: |||| | |||||||:|||||||:|||||||:|||:|:||| ||| |
 Db 61 YLQKPGQSPQLIYLGSNRASGVPDFSGSGSGTDFTLKISKVEAEDEVGIYYCMQGLQTP 120

 Qy 121 RTFGGGTKLEIK 132
 :||| |||:|||
 Db 121 QTFGQGTKVEIK 132

RESULT 7

AAH63599

ID AAH63599 PRELIMINARY; PRT; 239 AA.
 AC AAH63599;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;
Best Local Similarity 68.8%; Pred. No. 2.4e-37;
Matches 88; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 5 AQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQR 64
|| | ||:||: ::| :|||||||: ||:|||||||:||:||| | :| ||:|| |||
Db 5 AQLLGLLMLWVPGSSGDIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQR 64

Qy 65 PGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWFQGTHFPRTFG 124
|| | :| ||| :| |||||||:||||:|||||||:||||:||| | :|||||||
Db 65 PGQPPRLLIYKISNRFGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVSHFPRTFG 124

Qy 125 GGTKLEIK 132
| :| :| |||
Db 125 QGTRVEIK 132

RESULT 8
Q99M37
ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; D28195; D28195.
DR PIR; E28195; E28195.
DR PIR; F27887; F27887.
DR PIR; F32530; F32530.
DR PIR; JL0029; JL0029.
DR PIR; PH1035; PH1035.
DR PIR; PH1036; PH1036.
DR PIR; PH1037; PH1037.
DR PIR; PH1038; PH1038.
DR PIR; PH1039; PH1039.
DR PIR; PH1040; PH1040.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24498; S24498.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24502; S24502.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24506; S24506.
DR PIR; S24507; S24507.
DR PIR; S24508; S24508.
DR PIR; S24509; S24509.
DR PIR; S24510; S24510.
DR PIR; S24529; S24529.
DR PIR; S24530; S24530.
DR PIR; S24531; S24531.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24534; S24534.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24537; S24537.
DR PIR; S24538; S24538.
DR PIR; S24539; S24539.
DR PDB; 1I9I; X-ray; L=20-238.

DR PDB; 1I9J; X-ray; L=20-238.
 DR PDB; 1KTR; X-ray; L=17-132.
 DR PDB; 1LO2; X-ray; L/X=20-238.
 DR PDB; 1LO3; X-ray; L/X=20-238.
 DR PDB; 1LO4; X-ray; L=20-236.
 DR PDB; 2MPA; X-ray; L=20-238.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

 Query Match 66.5%; Score 460; DB 2; Length 238;
 Best Local Similarity 69.6%; Pred. No. 2.7e-36;
 Matches 87; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

 Qy 8 LFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSGKTYLNWLLQRPGQ 67
 | :|: || :: ||||||||:| |::| ||||:||||:|:| ||| | ||:|||
 Db 7 LLVLMFWIPASSSDVVMQTPLSLPVSLGDQASISCRSSQSVHSNGNTYLEWYLQKPGQ 66

 Qy 68 SPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCQGTHFPRTFGGGT 127
 ||| ||| || ||||||:|||||:|||||:|||||:|||:|||:|||:||| ||| |||
 Db 67 SPKLLIYKVSNRSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGT 126

 Qy 128 KLEIK 132
 |||||
 Db 127 KLEIK 131

RESULT 9
 Q8VCI6
 ID Q8VCI6 PRELIMINARY; PRT; 238 AA.
 AC Q8VCI6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR PIR; A27887; A27887.
DR PIR; A32248; A32248.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.
DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; E32530; E32530.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; PH1045; PH1045.
DR PIR; PL0257; PL0257.
DR PIR; PT0178; PT0178.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR PDB; 1A3R; X-ray; L=-.
DR PDB; 1ACY; X-ray; L=-.
DR PDB; 1H3P; X-ray; L=20-238.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

 Query Match 66.3%; Score 459; DB 2; Length 238;
 Best Local Similarity 70.4%; Pred. No. 3.4e-36;
 Matches 88; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

 QY 8 LFLLVLWIRETNGYVVMTQTPLTSLVTIGQPASISCKSSQSLSDGKTYLNWLLQRPGQ 67
 || :|: || :: |||||||:|| |::| |||||:||||: ||:| |||:| ||:|||
 Db 7 LLVLMFWIPASSSDVVMQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQ 66

 QY 68 SPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGT 127
 ||| ||| || |||||||:||||| |||:|||:|||:|||:|||:|||:|||:|||:|||:|||
 Db 67 SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGT 126

 QY 128 KLEIK 132
 |||||
 Db 127 KLEIK 131

RESULT 10

Q8VC55
 ID Q8VC55 PRELIMINARY; PRT; 239 AA.
 AC Q8VC55;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KC5; X-ray; L=21-239.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACAC25C337 CRC64;

Query Match 65.5%; Score 453; DB 2; Length 239;
Best Local Similarity 67.4%; Pred. No. 1.3e-35;
Matches 89; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| | : ||: :: ||:|||||:|| || ||||||||:|||:||| |||:
Db 1 MKLPVLLVVLLFTSPASSSDVVLQTPLSLPVNIGDQASISCKSTKSLLNSDGFTYLDW 60

Qy 61 LLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
||:|||||: ||||||| |||||||:||||||||||||:|||||:|||:|| | |
Db 61 YLQKPGQSPQLLIYLVSNRSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLP 120

Qy 121 RTFGGGTKLEIK 132
|||||||||||
Db 121 YTFGGGTKEIK 132

RESULT 11
BAC04905
ID BAC04905 PRELIMINARY; PRT; 239 AA.
AC BAC04905;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ39619 fis, clone SMINT2000984, highly similar to IG KAPPA
DE CHAIN V-II REGION GM607.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK096938; BAC04905.1; -.
SQ SEQUENCE 239 AA; 25964 MW; 78D9005B0E5CA51E CRC64;

Query Match 64.7%; Score 448; DB 2; Length 239;
Best Local Similarity 64.4%; Pred. No. 4e-35;
Matches 85; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| ||| | ||:||: ::| :|||:||:| || |:|||||:||| ||| |::| |::|
Db 1 MRLPAQLLGLMLWVSGSSGEIVMTQSPLSLPVTAGEPASISCRSSQSLLHSNGYNYVDW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
||:||||: ||:| | |||||||:||||||| |||||:||||:||:|:| | |
Db 61 YLQKPGQSPQLLIFLSSNRASGVPDFRSGSGSGTDFILKISRVEAEDVGVYFCMQALQMP 120

Qy 121 RTFGGGTKLEIK 132
||| |||:|||
Db 121 GTFGQGTTKVEIK 132

RESULT 12

Q9UL80

ID Q9UL80 PRELIMINARY; PRT; 114 AA.

AC Q9UL80;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; Q99M37; 1I9I.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 64.2%; Score 444.5; DB 2; Length 114;
Best Local Similarity 76.8%; Pred. No. 3.8e-35;
Matches 86; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
||||:||:|| ||: |||||||:|||| : ||| ||||| |||||||:|||| || |||
Db 2 VVMTQSPLSLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRKIEAEGLGLYYCWQGTHFPR-TFGGGTKLEIK 132
|||||:|||||:|||||:||||:||:||| ||||:| ||| |||:|||
Db 62 GVPDRFSGSGSGTDFTLKISRVEAEVGVYYCMQGTHWPPWTFGQGKVEIK 113

RESULT 13

Q6PIH6

ID Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC034142; AAH34142.1; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; C1-set; 1.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 63.8%; Score 441.5; DB 2; Length 240;

Best Local Similarity 66.2%; Pred. No. 1.7e-34;

Matches 88; Conservative 17; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| ||| | ||:||: ::| :|| |:||:|||| |:|||||||:|||||| |:| | :|

Db 1 MRLPAQLLGLMLWVGSSGDIVMAQSPLSLSVTPGEPASISCRSSQSLLHSNGNYFDW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHF- 119
||:|||||: ||| | |||||||:|||||||||:|||||:||:||| |

Db 61 YLQKPGQSPQLIYWGSNRASGVPDFRSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP 120

Qy 120 PRTFGGGTKLEIK 132
| ||| |||||||

Db 121 PYTFGQGTKLEIK 133

RESULT 14

AAH34142

ID AAH34142 PRELIMINARY; PRT; 240 AA.
AC AAH34142;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnérch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 63.8%; Score 441.5; DB 2; Length 240;
Best Local Similarity 66.2%; Pred. No. 1.7e-34;
Matches 88; Conservative 17; Mismatches 27; Indels 1; Gaps 1;

QY 1 MMSPAQFLFLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| ||| | ||:||: ::| :|| |:||:|||| |:||||||:|||||| |:| | :|
Db 1 MRLPAQLLGLMLWVGSSGDIVMAQSPLSLSVTPGEPASISCRSSQSLLHSNGNYFDW 60

QY 61 LIQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHF- 119

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Db      ||:|||||: |||  |||||||:|||||||||:||||:|:|||  |
61  YLQKPGQSPQLIYWGSNRASGVPDFSGSGSGTDFTLKISRVEAEDGVVYCMQALQTP. 120

Qy      120 PRTFGGGTKLEIK 132
Db      121 PYTFGQGTTKLEIK 133

```

RESULT 15

AAR11017

ID AAR11017 PRELIMINARY; PRT; 114 AA.
AC AAR11017;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY436857; AAR11017.1; -.
FT NON_TER 1 1
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12422 MW; C94A4DDCF55E8A8C CRC64;

Query Match 63.0%; Score 436; DB 2; Length 114;
Best Local Similarity 75.2%; Pred. No. 2.5e-34;
Matches 82; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Qy 24 MTQTPPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDGV 83
Db 1 MTQTPPLSPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGV 60

Qy 84 PDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 61 PDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGSHVPWTFGGGTKLEIK 109

Search completed: December 13, 2004, 19:17:44

Job time : 127.644 secs